Comparison between SEQ ID NO:4 and Q96PY6

FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAUTa4Xs: 1214 aa
 >seqid4
 vs /tmp/fastaDAAVTa4Xs library
searching /tmp/fastaDAAVTa4Xs library

   1258 residues in   1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 40, opt: 28, gap-pen: -12/ -2, width: 16
 Scan time: 0.034
The best scores are: opt
sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kin (1258) 4775

>>sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kinase N (1258 aa)
 initn: 4773 init1: 4773 opt: 4775
 Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

              10   20   30   40   50   60
seqid4 MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH
       ::
sp|Q96 MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH
              10   20   30   40   50   60

              70   80   90   100   110   120
seqid4 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFVQICLALKHVH
       ::
sp|Q96 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFVQICLALKHVH
              70   80   90   100   110   120

             130   140   150   160   170   180
seqid4 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY
       ::
sp|Q96 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY
             130   140   150   160   170   180

             190   200   210   220   230   240
seqid4 NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK
       ::
sp|Q96 NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK
             190   200   210   220   230   240

             250   260   270   280   290   300
seqid4 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSI
       ::
sp|Q96 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSI
             250   260   270   280   290   300

             310   320   330   340   350   360
seqid4 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISE
       ::

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            310       320       330       340       350       360
sp|Q96 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISE

            370       380       390       400       410       420
seqid4 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
            370       380       390       400       410       420

            430       440       450       460       470
seqid4 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPER---
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPERGIL
            430       440       450       460       470       480

                                                      480       490
seqid4 -------------------------------------------QKGQLAVERAKQVEEFLQR
                                                  ::::::::::::::::::::
sp|Q96 PGVRPGFPYGAAGHHHFPDADDIRKTLKRLKAVSKQANANRQKGQLAVERAKQVEEFLQR
            490       500       510       520       530       540

            500       510       520       530       540       550
seqid4 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
            550       560       570       580       590       600

            560       570       580       590       600       610
seqid4 RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE
            610       620       630       640       650       660

            620       630       640       650       660       670
seqid4 TGGSPSKQQMRSVISVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRLNENL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 TGGSPSKQQMRSVISVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRLNENL
            670       680       690       700       710       720

            680       690       700       710       720       730
seqid4 KAQEDEKGMQNLSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTLDTSFS
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 KAQEDEKGKQNLSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTLDTSFS
            730       740       750       760       770       780

            740       750       760       770       780       790
seqid4 TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAELQLQTELLENTTIRSEISPEG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAELQLQTELLENTTIRSEISPEG
            790       800       810       820       830       840

            800       810       820       830       840       850
seqid4 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLET
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLET
            850       860       870       880       890       900

            860       870       880       890       900       910
seqid4 EILQEPSGTNKDESLPCTITDVWISEEKETKETQSADRITIQENEVSEDGVSSTVDQLSD
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 EILQEPSGTNKDESLPCTITDVWISEEKETKETQSADRITIQENEVSEDGVSSTVDQLSD
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              910        920        930        940        950        960

         920        930        940        950        960        970
seqid4 IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH
                970        980        990       1000       1010       1020


         980        990       1000       1010       1020       1030
seqid4 LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEID
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEID
               1030       1040       1050       1060       1070       1080


        1040       1050       1060       1070       1080       1090
seqid4 EIKDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYSEEEESVLKNSDVEP
       :.:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 EIEDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYSEEEESVLKNSDVEP
               1090       1100       1110       1120       1130       1140


        1100       1110       1120       1130       1140       1150
seqid4 TANGTDVADEDDNPSSESALNEEWHSDNSDGEIASECECDSVFNHLEELRLHLEQEMGFE
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 TANGTDVADEDDNPSSESALNEEWHSDNSDGEIASECECDSVFNHLEELRLHLEQEMGFE
               1150       1160       1170       1180       1190       1200


        1160       1170       1180       1190       1200       1210
seqid4 KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
               1210       1220       1230       1240       1250
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